```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2009; month=3; day=12; hr=11; min=2; sec=14; ms=883; ]
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************************************************************
Reviewer Comments:
E287           Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
E287           Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151>
E287           Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151>


<140> 10/565,646
<141> March 24, 2006

<150> PCT/FR2004/001952
<151> July 22, 2004

<150> FR/09161
<151> July 25, 2003


Please change the format of the dates above to (YYYY-MM-DD).


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<212>  PRT
<213>  Bos taurus


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```

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Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu      210
               215                    220

Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala
225                    230                    235                    240
```

"The enumeration of amino acids shall start at the first amino acid as number 1. It shall be marked below the sequence every 5 amino acids. SEQ ID # 6 amino acid number 210 is not in the correct location. Please make all necessary changes.

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************************************************************
```

Application No: 10565646   Version No: 2.0

Input Set:

Output Set:

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Finished:	2009-02-05 20:47:46.221
Elapsed:	0 hr(s) 2 min(s) 32 sec(s) 471 ms
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Total Errors:	335
No. of SeqIDs Defined:	11
Actual SeqID Count:	11

Error code		Error Description
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E	287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151>
E	201	Mandatory field data missing in <223> in SEQ ID (1)
E	201	Mandatory field data missing in <223> in SEQ ID (1)
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E	201	Mandatory field data missing in <223> in SEQ ID (1)
E	320	Wrong Nucleic Acid Designator, ga in SEQID (1)
E	320	Wrong Nucleic Acid Designator, gt in SEQID (1)
E	320	Wrong Nucleic Acid Designator, gg in SEQID (1)
E	320	Wrong Nucleic Acid Designator, ac in SEQID (1)
E	320	Wrong Nucleic Acid Designator, gc in SEQID (1)
E	323	Invalid/missing amino acid numbering SEQID (1) POS (6764)

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                    Input Set:


                    Output Set:


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              Total Warnings:    21
                Total Errors:    335
        No. of SeqIDs Defined:   11
           Actual SeqID Count:   11


   Error code      Error Description

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   E   320      Wrong Nucleic Acid Designator,    gg   in SEQID (1)

   E   320      Wrong Nucleic Acid Designator,    ag   in SEQID (1)

   E   201      Mandatory field data missing in <223>  in SEQ ID (3)

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   E   201      Mandatory field data missing in <223>  in SEQ ID (3)

   E   201      Mandatory field data missing in <223>  in SEQ ID (3)

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                This error has occured more than 20 times, will not be displayed

   E   320      Wrong Nucleic Acid Designator,    ga   in SEQID (3)

   E   320      Wrong Nucleic Acid Designator,    gt   in SEQID (3)

   E   320      Wrong Nucleic Acid Designator,    gg   in SEQID (3)

   E   322      CDS location out of range SEQID (3)  At Protien count (157)

   E   259      Found undefined lettercode; POS (4557) SEQID(3)

   E   259      Found undefined lettercode; POS (4558) SEQID(3)

   E   259      Found undefined lettercode; POS (4559) SEQID(3)

   E   259      Found undefined lettercode; POS (4560) SEQID(3)

   E   254      The total number of bases conflicts with running total, Input:
                4616,  Calculated : 4620 SEQID(3)
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```
                    Input Set:


                    Output Set:


                     Started:   2009-02-05 20:45:13.750
                    Finished:   2009-02-05 20:47:46.221
                     Elapsed:   0 hr(s) 2 min(s) 32 sec(s) 471 ms
              Total Warnings:   21
                Total Errors:   335
       No. of SeqIDs Defined:   11
           Actual SeqID Count: 11
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Error code	Error Description
E 254	The total number of bases conflicts with running total, Input: 4676, Calculated : 4680 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4734, Calculated : 4738 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4782, Calculated : 4786 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4830, Calculated : 4834 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4878, Calculated : 4882 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4926, Calculated : 4930 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 4974, Calculated : 4978 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5022, Calculated : 5026 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5070, Calculated : 5074 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5118, Calculated : 5122 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5166, Calculated : 5170 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5214, Calculated : 5218 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5262, Calculated : 5266 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5310, Calculated : 5314 SEQID(3)
E 254	The total number of bases conflicts with running total, Input: 5358, Calculated : 5362 SEQID(3)

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                      Input Set:


                     Output Set:



                       Started:   2009-02-05 20:45:13.750
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                Total Warnings:   21
                  Total Errors:   335
       No. of SeqIDs Defined:    11
          Actual SeqID Count:    11


  Error code      Error Description


  E   254         The total number of bases conflicts with running total, Input:
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  E   254         The total number of bases conflicts with running total, Input:
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  E   254         The total number of bases conflicts with running total, Input:
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  E   254         The total number of bases conflicts with running total, Input:
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                   This error has occured more than 20 times, will not be displayed

  E   320         Wrong Nucleic Acid Designator,   gc   in SEQID (3)

  E   322         CDS location out of range SEQID (3)  At Protien count (476)

  E   323         Invalid/missing amino acid numbering  SEQID (3)  POS (6768)

  E   322         CDS location out of range SEQID (3)  At Protien count (505)

  E   320         Wrong Nucleic Acid Designator,   gg   in SEQID (3)

  E   322         CDS location out of range SEQID (3)  At Protien count (573)

  E   320         Wrong Nucleic Acid Designator,   gg   in SEQID (3)

  E   322         CDS location out of range SEQID (3)  At Protien count (603)

  E   320         Wrong Nucleic Acid Designator,   ag   in SEQID (3)

  E   322         CDS location out of range SEQID (3)  At Protien count (649)

  E   253         The number of bases differs from <211> Input: 8146

  E   323         Invalid/missing amino acid numbering  SEQID (5) POS (2323)

  E   320         Wrong Nucleic Acid Designator,   ga   in SEQID (5)

  E   320         Wrong Nucleic Acid Designator,   gt   in SEQID (5)

  E   323         Invalid/missing amino acid numbering  SEQID (5) POS (4694)

  E   320         Wrong Nucleic Acid Designator,   ac   in SEQID (5)
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Error code		Error Description
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E	320	Wrong Nucleic Acid Designator, ag in SEQID (5) This error has occured more than 20 times, will not be displayed
W	112	Upper case found in data; Found at position(0) SeqId(6)
W	112	Upper case found in data; Found at position(3) SeqId(6)
E	259	Found undefined lettercode; POS (6) SEQID(6)
W	112	Upper case found in data; Found at position(6) SeqId(6)
E	259	Found undefined lettercode; POS (8) SEQID(6)
E	342	'n' position not defined found at POS: 9 SEQID(6)
W	112	Upper case found in data; Found at position(9) SeqId(6)
E	259	Found undefined lettercode; POS (12) SEQID(6)
W	112	Upper case found in data; Found at position(12) SeqId(6)
E	259	Found undefined lettercode; POS (15) SEQID(6)
W	112	Upper case found in data; Found at position(15) SeqId(6)
E	259	Found undefined lettercode; POS (18) SEQID(6)
W	112	Upper case found in data; Found at position(18) SeqId(6)
E	259	Found undefined lettercode; POS (20) SEQID(6)
W	112	Upper case found in data; Found at position(21) SeqId(6)
E	259	Found undefined lettercode; POS (24) SEQID(6)
W	112	Upper case found in data; Found at position(24) SeqId(6)
E	259	Found undefined lettercode; POS (26) SEQID(6)
W	112	Upper case found in data; Found at position(27) SeqId(6)
E	259	Found undefined lettercode; POS (30) SEQID(6)

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                    Input Set:


                    Output Set:



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              Total Errors:     335
      No. of SeqIDs Defined:    11
          Actual SeqID Count:   11
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Error code		Error Description
W	112	Upper case found in data; Found at position(30) SeqId(6)
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W	112	Upper case found in data; Found at position(33) SeqId(6)
E	259	Found undefined lettercode; POS (35) SEQID(6)
E	342	'n' position not defined found at POS: 36 SEQID(6)
W	112	Upper case found in data; Found at position(36) SeqId(6)
E	259	Found undefined lettercode; POS (38) SEQID(6)
W	112	Upper case found in data; Found at position(39) SeqId(6)
E	259	Found undefined lettercode; POS (41) SEQID(6)
E	342	'n' position not defined found at POS: 42 SEQID(6)
W	112	Upper case found in data; Found at position(42) SeqId(6)
E	259	Found undefined lettercode; POS (44) SEQID(6)
W	112	Upper case found in data; Found at position(45) SeqId(6)
E	259	Found undefined lettercode; POS (47) SEQID(6)
E	259	Found undefined lettercode; POS (49) SEQID(6) This error has occured more than 20 times, will not be displayed
E	323	Invalid/missing amino acid numbering SEQID (6) POS (209)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (210)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (214)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (215)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (219)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (220)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (224)

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            Input Set:


           Output Set:


             Started:    2009-02-05 20:45:13.750
            Finished:    2009-02-05 20:47:46.221
             Elapsed:    0 hr(s) 2 min(s) 32 sec(s) 471 ms
      Total Warnings:    21
        Total Errors:    335
No. of SeqIDs Defined:   11
   Actual SeqID Count:   11
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Error code	Error Description
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E 323	Invalid/missing amino acid numbering SEQID (6) POS (229)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (230)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (234)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (235)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (239)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (240)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (244)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (245) This error has occured more than 20 times, will not be displayed
E 331	Count of Protein differs from the <211> tag Input: 648
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (11)

SEQUENCE LISTING

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 Julien, Raymond
 Lafort, Marie-Piere,
 Leveziel, Hubert

<120> USE OF THE SILVER GENE FOR THE AUTHENTIFICATION OF
       THE ORIGINAL BREED OF ANIMAL POPULATIONS AND
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<130> 0508-1156

<140> 10565646
<141> 2006-03-24

<150> PCT/FR2004/001952
<151> July 22, 2004

<150> FR/09161
<151> July 25, 2003

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Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr
    10              15                  20

gaa g gtgagtgtgg gatgttggac atgaacaagt gtgaatttgg ggttgcacac       155
Glu
25

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Ser Gln Gly Pro Asp Cys Trp Arg
55               60


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Ile Asn
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tgactccttc ctcttccaca gcacctagtc aactctatta tacttctttc tgggagccct    4118
gctccaatta tagtcccatc ccatggaccc tctcataagg actttttcc tgcccaacat     4178
atgcaagctt aaactcctg aaataaccat ccttgataca tctcctgacc ttccttctct     4238
ggttccatct ctaaccctgc cccagtctcc tttgaccagt aacccccttc cctactcttc    4298

tttccaaaaa cctcag ac  caa tac tgg caa gtt ctg ggg ggc cca gtg tct   4349
                       Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser
                                     160              165

gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg     4397
Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met
     170              175              180

gaa gtg act gtc tac cac cgc cgg ggg tcc cag agc tat gtg ccc ctc     4445
Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu
185              190              195              200

gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggaggggac      4496
Ala His Ser Ser Ser Ala Phe Thr Ile Thr
                   205              210

aaggccagtt gcagggcagg agaaggtggg gaggctgggc tggacaggaa aggggaaaga    4556
ggaaatggtg tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg    4616
gcttggagcc cgtgaagggc caggcagctt gggttggttg aaaaatatgg ctgtgaaaga    4676
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agaagctgac agaaagaaga acttatggtt ctcactttct ctgactccaa tcccag ac      4734
                                                           Asp


cag gtg ccc ttc tct gtg agt gtg tct cag ctg cag gcc ttg gat gga      4782
Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Leu Ala Leu Asp Gly
            215             220             225


agg aac aag cgc ttc ctg aga aag cag cct ctg acc ttt gcc ctc cag      4830
Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln
        230             235             240


ctc cat gat ccc agt ggc tat ttg gct ggg gct gac ctt tcc tac acc      4878
Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr
        245             250             255


tgg gac ttt ggt gac agt aca ggg acc ctg atc tct cgg gca ctc acg      4926
Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr
260             265             270             275


gtc act cac act tac cta gag tct ggc cca gtc act gca cag gtg gtg      4974
Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val
            280             285             290


ctg cag gct gcc att cct ctc acc tcc tgt ggc tcc tca cca gtt cca      5022
Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro
            295             300             305




ggc act aca gat agg cat gtg aca act gca gag gct cct gga acc aca      5070
Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr
        310             315             320


gct ggc caa gtg cct act aca gaa gtc atg ggc acc aca cct ggc cag      5118
Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr Pro Gly Gln
        325             330             335


gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc      5166
Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr
340             345             350             355


aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc      5214
Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr Ser Lys Val
            360             365             370


tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg      5262
Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr Gly Arg
        375             380             385


aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag      5310
Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val Thr Gln
        390             395             400


gga aca act cca cag ctg gtg gag acc aca gct gga gag gtg tcc act      5358
Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr
    405             410             415
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cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt      5406
Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr Glu Gly
420              425              430              435

act gca g gtaaggggggc caccatgaat gagttcatag aggtggggca tttgtcacag     5463
Thr Ala


ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag    5523
tggagtcccc tcagaatctt cactggtttt aaaaccccct aagtccctct taatggcaca    5583
gaatagatcc agagttcagg aaaccagggt cttctcctag gccaggggta gagagcttat    5613
tctctcttcc tgaagagaag ttcaggaagc agtgtgtgat catttggtgg tggtgctcag    5703
tcatgtctga ctctttgtga cctcatggac tatggcccac caggctcctc tgtccataga    5763
attctccagg caagaacact ggagtgggtg gccatttcct tctccagggg attttccctg    5823
cccagggatt aaacccgaat tggcaggtgg attctttacc cgagccacct agaaagtccc    5883
atgtgatcat tagataatac ttatacctca ttttctgatt aagtgtaaac acagaaatct    5943
ttctgacacc acttcccacc cctggattcc catcccaaag taggtttacc tggaattgtg    6003
gtaggaatac taaaaaggga gaagtgagat agtgacacta tgacttaaca catgtcaaat    6063
gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaaattc   6123
tgactctaac cctgtgactc tggggcagtc atttctcttg ggcctttctt tatcttaaaa    6183
aatgagagtt tccagctctt gtctgattct aagcctggat ccagtagctc tgactctacc   6243
tggaaaaatg cttgttgggc ctgtttttcag gttagtcatt tgcttttttga ctttgcctct   6303


ttaatcctct cctccag gc  tcc ctg agt ccc ctg ccg gat gac act gcc        6352
                     Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala
                           440              445


acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat       6400
Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr
   450              455              460


cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg          6447
Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val
465              470              475


cctacattgt ccgtaagctg gtggaggggag gcgtgtgctg cttaggggttg cccagtggaa  6507
gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggtttc    6567
atatgaaggc agaatgggat tagggaggca gcccgaggac cttcctggcc atgggccttg    6627


gggggaggata agtagaggag tctcagactt aaaaaaaatct tgcaactttg cag ag       6682
                                                              Gln


ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga       6730
Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly
    480              485              490


gat gca ttt gag ctg act gtg tct tgc caa ggc gg  gtgagtgtcc           6775
Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly
    495              500


cacggttgcc ctgagaactc ctggggtgac tgctgtcctg ttctctggtg tctagtgtcc    6835


cttcccagat tccctgacgt aagctgacat ctctcccag g cta ccc aag gaa gcc     6890
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                                      Leu Pro Lys Glu Ala
                                                  510


tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg    6938
Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu
                515                 520                 525


tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag    6986
Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln
            530                 535                 540


gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct    7034
Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala
            545                 550                 555


gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g      7080
Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro
        560                 565                 570


gtaggtagtt ggacaagagg taggatgaag acacggggag atggtagagg ttacctacta   7140


gaggaagcag acactgaatg cagccgtatc tgggattcca cccatag gg  caa gaa     7195
                                                     Gly Gln Glu
                                                             575


gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta    7243
Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu
            580                 585                 590


aca gct ttg ttg ctt gca tct ctg ata tac ag  gtgagatccc cgccatcctg   7295
Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg
            595                 600


ctcccactcc tttacccctt attaccacca ccactcttcc tcatgggaag aagaaac
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